## Michelle R Lacey

List of Publications by Year in descending order

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201385 214527 2,362 54 27 47 citations h-index g-index papers 60 60 60 4228 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	In Vitro High-Capacity Assay to Quantify the Clonal Heterogeneity in Trilineage Potential of Mesenchymal Stem Cells Reveals a Complex Hierarchy of Lineage Commitment. Stem Cells, 2010, 28, 788-798.	1.4	376
2	DNA methylation and differentiation: silencing, upregulation and modulation of gene expression. Epigenomics, 2013, 5, 553-568.	1.0	176
3	Differences in Gastric Carcinoma Microenvironment Stratify According to EBV Infection Intensity: Implications for Possible Immune Adjuvant Therapy. PLoS Pathogens, 2013, 9, e1003341.	2.1	140
4	DNA Hypomethylation and Hemimethylation in Cancer. Advances in Experimental Medicine and Biology, 2013, 754, 31-56.	0.8	126
5	Adult human mesenchymal stem cells enhance breast tumorigenesis and promote hormone independence. Breast Cancer Research and Treatment, 2010, 121, 293-300.	1.1	101
6	Early de novo DNA methylation and prolonged demethylation in the muscle lineage. Epigenetics, 2013, 8, 317-332.	1.3	85
7	Gene expression during normal and FSHD myogenesis. BMC Medical Genomics, 2011, 4, 67.	0.7	81
8	Serum Cadmium Levels in Pancreatic Cancer Patients from the East Nile Delta Region of Egypt. Environmental Health Perspectives, 2006, 114, 113-119.	2.8	76
9	Decompressive Craniectomy for Elevated Intracranial Pressure and Its Effect on the Cumulative Ischemic Burden and Therapeutic Intensity Levels After Severe Traumatic Brain Injury. Neurosurgery, 2010, 66, 1111-1119.	0.6	73
10	Clonal analysis of the proliferation potential of human bone marrow mesenchymal stem cells as a function of potency. Biotechnology and Bioengineering, 2011, 108, 2716-2726.	1.7	70
11	High-Resolution Rapid Diagnostic Imaging of Whole Prostate Biopsies Using Video-Rate Fluorescence Structured Illumination Microscopy. Cancer Research, 2015, 75, 4032-4041.	0.4	66
12	Association of 5-hydroxymethylation and 5-methylation of DNA cytosine with tissue-specific gene expression. Epigenetics, 2017, 12, 123-138.	1.3	61
13	Epigenetics of a tandem DNA repeat: chromatin DNasel sensitivity and opposite methylation changes in cancers. Nucleic Acids Research, 2008, 36, 2196-2207.	6.5	51
14	DNA methylation and differentiation: HOX genes in muscle cells. Epigenetics and Chromatin, 2013, 6, 25.	1.8	49
15	Notch signaling genes. Epigenetics, 2014, 9, 842-850.	1.3	49
16	Identification of a novel mitogen-activated protein kinase in Toxoplasma gondii. International Journal for Parasitology, 2004, 34, 1245-1254.	1.3	40
17	Both Hypomethylation and Hypermethylation in a 0.2-kb Region of a DNA Repeat in Cancer. Molecular Cancer Research, 2005, 3, 617-626.	1.5	40
18	Cell-Surface Expression of Neuron-Glial Antigen 2 (NG2) and Melanoma Cell Adhesion Molecule (CD146) in Heterogeneous Cultures of Marrow-Derived Mesenchymal Stem Cells. Tissue Engineering - Part A, 2013, 19, 2253-2266.	1.6	40

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19	RNA CoMPASS: A Dual Approach for Pathogen and Host Transcriptome Analysis of RNA-Seq Datasets. PLoS ONE, 2014, 9, e89445.	1.1	38
20	Hyperbaric Oxygen Promotes Proximal Bone Regeneration and Organized Collagen Composition during Digit Regeneration. PLoS ONE, 2015, 10, e0140156.	1.1	38
21	Toxoplasma gondii Expresses Two Mitogen-Activated Protein Kinase Genes That Represent Distinct Protozoan Subfamilies. Journal of Molecular Evolution, 2007, 64, 4-14.	0.8	36
22	Endocrine disrupting chemicals in New Orleans surface waters and Mississippi Sound sediments. Journal of Environmental Monitoring, 2012, 14, 1353.	2.1	34
23	Expression profiling using a hexamer-based universal microarray. Nature Biotechnology, 2004, 22, 418-426.	9.4	33
24	A signal-to-noise analysis of phylogeny estimation by neighbor-joining: Insufficiency of polynomial length sequences. Mathematical Biosciences, 2006, 199, 188-215.	0.9	32
25	Hemimethylation footprints of DNA demethylation in cancer. Epigenetics, 2009, 4, 165-175.	1.3	32
26	Developmentally linked human DNA hypermethylation is associated with down-modulation, repression, and upregulation of transcription. Epigenetics, 2018, 13, 275-289.	1.3	31
27	Tissue-specific epigenetics of atherosclerosis-related <i>ANGPT</i> and <i>ANGPTL</i> genes. Epigenomics, 2019, 11, 169-186.	1.0	30
28	Atherosclerosis-associated differentially methylated regions can reflect the disease phenotype and are often at enhancers. Atherosclerosis, 2019, 280, 183-191.	0.4	29
29	Expanding Research Capacity in Sub-Saharan Africa Through Informatics, Bioinformatics, and Data Science Training Programs in Mali. Frontiers in Genetics, 2019, 10, 331.	1.1	26
30	An Ex Vivo Model for Anti-Angiogenic Drug Testing on Intact Microvascular Networks. PLoS ONE, 2015, 10, e0119227.	1.1	23
31	Epigenetics of Skeletal Muscle-Associated Genes in the ASB, LRRC, TMEM, and OSBPL Gene Families. Epigenomes, 2020, 4, 1.	0.8	23
32	Modeling, simulation and analysis of methylation profiles from reduced representation bisulfite sequencing experiments. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 723-42.	0.2	22
33	Epigenetics of the myotonic dystrophy-associated <i>DMPK</i> gene neighborhood. Epigenomics, 2016, 8, 13-31.	1.0	22
34	DNA Hypomethylation in Intragenic and Intergenic Enhancer Chromatin of Muscle-Specific Genes Usually Correlates with their Expression. Yale Journal of Biology and Medicine, 2016, 89, 441-455.	0.2	22
35	Tissue-specific epigenetics in gene neighborhoods: myogenic transcription factor genes. Human Molecular Genetics, 2015, 24, 4660-4673.	1.4	21
36	A Comparison of Clinical and Pathologic Assessments for the Prediction of Occult Nipple Involvement in Nipple-Sparing Mastectomies. Annals of Surgical Oncology, 2013, 20, 128-132.	0.7	18

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37	Epigenetics and expression of key genes associated with cardiac fibrosis: <i>NLRP3, MMP2, MMP9, CCN2/CTGF</i> and <i>AGT</i> Epigenomics, 2021, 13, 219-234.	1.0	16
38	Myogenic Differential Methylation: Diverse Associations with Chromatin Structure. Biology, 2014, 3, 426-451.	1.3	15
39	Identification of biomarkers for tuberculosis susceptibility via integrated analysis of gene expression and longitudinal clinical data. Frontiers in Genetics, 2014, 5, 240.	1.1	14
40	TgMAPK1 is a Toxoplasma gondii MAP kinase that hijacks host MKK3 signals to regulate virulence and interferon- $\hat{l}^3$ -mediated nitric oxide production. Experimental Parasitology, 2013, 134, 389-399.	0.5	13
41	Sirtuin 3 deficiency does not impede digit regeneration in mice. Scientific Reports, 2019, 9, 16491.	1.6	13
42	Modeling Dependence in Methylation Patterns with Application to Ovarian Carcinomas. Statistical Applications in Genetics and Molecular Biology, 2009, 8, 1-27.	0.2	12
43	Quantitative Proteomic Analysis of the <i>Anopheles gambiae</i> (Diptera: Culicidae) Midgut Infected With O'nyong–Nyong Virus. Journal of Medical Entomology, 2013, 50, 1077-1088.	0.9	12
44	BRAFTesting in Multifocal Papillary Thyroid Carcinoma. BioMed Research International, 2015, 2015, 1-7.	0.9	12
45	Spatial transcriptomics reveals metabolic changes underly age-dependent declines in digit regeneration. ELife, $0,11,.$	2.8	12
46	Data showing atherosclerosis-associated differentially methylated regions are often at enhancers. Data in Brief, 2019, 23, 103812.	0.5	9
47	An Ex Vivo Tissue Culture Model for Anti-angiogenic Drug Testing. Methods in Molecular Biology, 2016, 1464, 85-95.	0.4	8
48	Deciphering transcription dysregulation in FSH muscular dystrophy. Journal of Human Genetics, 2012, 57, 477-484.	1.1	5
49	Age-Dependent Changes in Bone Architecture, Patterning, and Biomechanics During Skeletal Regeneration. Frontiers in Cell and Developmental Biology, 2021, 9, 749055.	1.8	5
50	Modeling Methylation Patterns with Long Read Sequencing Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1379-1389.	1.9	3
51	High-capacity assay to quantify the clonal heterogeneity in potency of mesenchymal stem cells. BMC Proceedings, 2011, 5, O14.	1.8	1
52	Plasma flow distal to tourniquet placement provides a physiological mechanism for tissue salvage. PLoS ONE, 2020, 15, e0244236.	1.1	1
53	A Sharp Error Probability Estimate for the Reconstruction of Phylogenetic Quartets by the Four-Point Method. Journal of Computational Biology, 2009, 16, 443-456.	0.8	0
54	Highâ€Capacity Assay to Evaluate Colonyâ€Forming Efficiency and Multipotency of Bone Marrow Stromal Cells. FASEB Journal, 2009, 23, LB247.	0.2	0